

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Boyle, William J.
- (ii) TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS
- (iii) NUMBER OF SEQUENCES: 7
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Amgen Inc.
  - (B) STREET: 1840 Dehavilland Drive
  - (C) CITY: Thousand Oaks
  - (D) STATE: California
  - (E) COUNTRY: USA
  - (F) ZIP: 91230-1789
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Winter, Robert B.
  - (C) REFERENCE/DOCKET NUMBER: A-451D

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 52 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTTCCTCCTCA TATGGATCCA AACCGTATTT CTGAAGACAG CACTCACTGC TT

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(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TACGCACTCC GCGGTTAGTC TATGTCCTGA ACTTTGA

37

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 53 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTTCTCCTCA TATGAAACCT GAAGCTCAAC CATTTGCACA CCTCACCATC AAT

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(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 45 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTTCTCCTCA TATGCATTTA ACTATTAACG CTGCATCTAT CCCAT

45

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 59 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTTCTCCTCA TATGACTATT AACGCTGCAT CTATCCCATC GGGTTCCCAT AAAGTCACT

59

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2295 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(B) LOCATION: 158..1105

GAGCTCGGAT	CCACTACTCG	ACCCACGCGT	CCGGCCAGGA	CCTCTGTGAA	CCGGTCGGGG		60									
CGGGGGCCGC	CTGGCCGGGA	GTCTGCTCGG	CGGTGGGTGG	CCGAGGAAGG	GAGAGAACGA		120									
TCGCGGAGCA	GGGCGCCCCA	ACTCCGGGCG	CCGCGCC	ATG Met	CGC Arg	CGG Arg	GCC Ala	AGC Ser	CGA Arg		175					
				1					5							
GAC Asp	TAC Tyr	GGC Gly	AAG Lys	TAC Tyr	CTG Leu	CGC Arg	AGC Ser	TCG Ser	GAG Glu	GAG Glu	ATG Met	GGC Gly	AGC Ser	GGC Gly	CCC Pro	223
			10					15					20			
GGC Gly	GTC Val	CCA Pro	CAC His	GAG Glu	GGT Gly	CCG Pro	CTG Leu	CAC His	CCC Pro	GCG Ala	CCT Pro	TCT Ser	GCA Ala	CCG Pro	GCT Ala	271
			25				30					35				
CCG Pro	GCG Ala	CCG Pro	CCA Pro	CCC Pro	GCC Ala	GCC Ala	TCC Ser	CGC Arg	TCC Ser	ATG Met	TTC Phe	CTG Leu	GCC Ala	CTC Leu	CTG Leu	319
			40				45				50					
GGG Gly	CTG Leu	GGA Gly	CTG Leu	GGC Gly	CAG Gln	GTG Val	GTC Val	TGC Cys	AGC Ser	ATC Ile	GCT Ala	CTG Leu	TTC Phe	CTG Leu	TAC Tyr	367
					60					65					70	
TTT Phe	CGA Arg	GCG Ala	CAG Gln	ATG Met	GAT Asp	CCT Pro	AAC Asn	AGA Arg	ATA Ile	TCA Ser	GAA Glu	GAC Asp	AGC Ser	ACT Thr	CAC His	415
				75					80					85		
TGC Cys	TTT Phe	TAT Tyr	AGA Arg	ATC Ile	CTG Leu	AGA Arg	CTC Leu	CAT His	GAA Glu	AAC Asn	GCA Ala	GGT Gly	TTG Leu	CAG Gln	GAC Asp	463
			90					95					100			
TCG Ser	ACT Thr	CTG Leu	GAG Glu	AGT Ser	GAA Glu	GAC Asp	ACA Thr	CTA Leu	CCT Pro	GAC Asp	TCC Ser	TGC Cys	AGG Arg	AGG Arg	ATG Met	511
			105				110					115				
AAA Lys	CAA Gln	GCC Ala	TTT Phe	CAG Gln	GGG Gly	GCC Ala	GTG Val	CAG Gln	AAG Lys	GAA Glu	CTG Leu	CAA Gln	CAC His	ATT Ile	GTG Val	559
			120				125				130					
GGG Gly	CCA Pro	CAG Gln	CGC Arg	TTC Phe	TCA Ser	GGA Gly	GCT Ala	CCA Pro	GCT Ala	ATG Met	ATG Met	GAA Glu	GGC Gly	TCA Ser	TGG Trp	607
					140					145					150	
TTG Leu	GAT Asp	GTG Val	GCC Ala	CAG Gln	CGA Arg	GGC Gly	AAG Lys	CCT Pro	GAG Glu	GCC Ala	CAG Gln	CCA Pro	TTT Phe	GCA Ala	CAC His	655
				155					160					165		
CTC Leu	ACC Thr	ATC Ile	AAT Asn	GCT Ala	GCC Ala	AGC Ser	ATC Ile	CCA Pro	TCG Ser	GGT Gly	TCC Ser	CAT His	AAA Lys	GTC Val	ACT Thr	703
			170					175					180			
CTG Leu	TCC Ser	TCT Ser	TGG Trp	TAC Tyr	CAC His	GAT Asp	CGA Arg	GGC Gly	TGG Trp	GCC Ala	AAG Lys	ATC Ile	TCT Ser	AAC Asn	ATG Met	751
			185				190					195				
ACG Thr	TTA Leu	AGC Ser	AAC Asn	GGA Gly	AAA Lys	CTA Leu	AGG Arg	GTT Val	AAC Asn	CAA Gln	GAT Asp	GGC Gly	TTC Phe	TAT Tyr	TAC Tyr	799
			200			205					210					

CTG Leu 215	TAC Tyr	GCC Ala	AAC Asn	ATT Ile	TGC Cys 220	TTT Phe	CGG Arg	CAT His	CAT His	GAA Glu 225	ACA Thr	TCG Ser	GGA Gly	AGC Ser	GTA Val 230	847
CCT Pro	ACA Thr	GAC Asp	TAT Tyr	CTT Leu 235	CAG Gln	CTG Leu	ATG Met	GTG Val	TAT Tyr 240	GTC Val	GTT Val	AAA Lys	ACC Thr	AGC Ser 245	ATC Ile	895
AAA Lys	ATC Ile	CCA Pro	AGT Ser 250	TCT Ser	CAT His	AAC Asn	CTG Leu 255	ATG Met	AAA Lys	GGA Gly	GGG Gly	AGC Ser	ACG Thr 260	AAA Lys	AAC Asn	943
TGG Trp	TCG Ser	GGC Gly 265	AAT Asn	TCT Ser	GAA Glu	TTC Phe	CAC His 270	TTT Phe	TAT Tyr	TCC Ser	ATA Ile	AAT Asn 275	GTT Val	GGG Gly	GGA Gly	991
TTT Phe 280	TTC Phe	AAG Lys	CTC Leu	CGA Arg	GCT Ala	GGT Gly 285	GAA Glu	GAA Glu	ATT Ile	AGC Ser	ATT Ile 290	CAG Gln	GTG Val	TCC Ser	AAC Asn	1039
CCT Pro 295	TCC Ser	CTG Leu	CTG Leu	GAT Asp	CCG Pro 300	GAT Asp	CAA Gln	GAT Asp	GCG Ala	ACG Thr 305	TAC Tyr	TTT Phe	GGG Gly	GCT Ala	TTC Phe 310	1087
AAA Lys	GTT Val	CAG Gln	GAC Asp	ATA Ile 315	GAC Asp	TGAGACTCAT TTCGTGGAAC ATTAGCATGG										1135
ATGTCCTAGA				TGTTTGAAA		CTTCTTAAAA		AATGGATGAT			GTCTATACAT		GTGTAAGACT			1195
ACTAAGAGAC				ATGGCCCACG		GTGTATGAAA		CTCACAGCCC			TCTCTCTTGA		GCCTGTACAG			1255
GTTGTGTATA				TGTAAGTCC		ATAGGTGATG		TTAGATTCAT			GGTGATTACA		CAACGGTTTTT			1315
ACAATTTTGT				AATGATTTCC		TAGAATTGAA		CCAGATTGGG			AGAGGTATTC		CGATGCTTAT			1375
GAAAACTTA				CACGTGAGCT		ATGGAAGGGG		GTCACAGTCT			CTGGGTCTAA		CCCCTGGACA			1435
TGTGCCACTG				AGAACCTTGA		AATTAAGAGG		ATGCCATGTC			ATTGCAAAGA		AATGATAGTG			1495
TGAAGGGTTA				AGTTCTTTTG		AATTGTTACA		TTGCGCTGGG			ACCTGCAAAT		AAGTTCTTTT			1555
TTTCTAATGA				GGAGAGAAAA		ATATATGTAT		TTTTATATAA			TGTCTAAAGT		TATATTTTCTAG			1615
GTGTAATGTT				TTCTGTGCAA		AGTTTTGTAA		ATTATATTTG			TGCTATAGTA		TTTGATTCAA			1675
AATATTTTAAA				AATGTCTCAC		TGTTGACATA		TTTAATGTTT			TAAATGTACA		GATGTATTTA			1735
ACTGGTGCAC				TTTGTAATTC		CCCTGAAGGT		ACTCGTAGCT			AAGGGGGCAG		AATACTGTTT			1795
CTGGTGACCA				CATGTAGTTT		ATTTCTTTTAT		TCTTTTTTAAC			TTAATAGAGT		CTTCAGACTT			1855
GTCAAAACTA				TGCAAGCAAA		ATAAATAAAT		AAAAATAAAA			TGAATACCTT		GAATAATAAG			1915

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met 1	Arg	Arg	Ala	Ser 5	Arg	Asp	Tyr	Gly	Lys 10	Tyr	Leu	Arg	Ser	Ser 15	Glu
Glu	Met	Gly	Ser 20	Gly	Pro	Gly	Val	Pro 25	His	Glu	Gly	Pro	Leu 30	His	Pro
Ala	Pro	Ser 35	Ala	Pro	Ala	Pro	Ala 40	Pro	Pro	Pro	Ala	Ala 45	Ser	Arg	Ser
Met	Phe 50	Leu	Ala	Leu	Leu	Gly 55	Leu	Gly	Leu	Gly	Gln 60	Val	Val	Cys	Ser
Ile 65	Ala	Leu	Phe	Leu	Tyr 70	Phe	Arg	Ala	Gln	Met 75	Asp	Pro	Asn	Arg	Ile 80
Ser	Glu	Asp	Ser	Thr 85	His	Cys	Phe	Tyr	Arg 90	Ile	Leu	Arg	Leu	His 95	Glu
Asn	Ala	Gly	Leu 100	Gln	Asp	Ser	Thr	Leu 105	Glu	Ser	Glu	Asp	Thr 110	Leu	Pro
Asp	Ser	Cys 115	Arg	Arg	Met	Lys	Gln 120	Ala	Phe	Gln	Gly	Ala 125	Val	Gln	Lys
Glu	Leu 130	Gln	His	Ile	Val	Gly 135	Pro	Gln	Arg	Phe	Ser 140	Gly	Ala	Pro	Ala
Met 145	Met	Glu	Gly	Ser	Trp 150	Leu	Asp	Val	Ala	Gln 155	Arg	Gly	Lys	Pro	Glu 160
Ala	Gln	Pro	Phe	Ala 165	His	Leu	Thr	Ile	Asn 170	Ala	Ala	Ser	Ile	Pro 175	Ser
Gly	Ser	His	Lys 180	Val	Thr	Leu	Ser	Ser 185	Trp	Tyr	His	Asp	Arg 190	Gly	Trp
Ala	Lys	Ile 195	Ser	Asn	Met	Thr	Leu 200	Ser	Asn	Gly	Lys	Leu 205	Arg	Val	Asn
Gln	Asp 210	Gly	Phe	Tyr	Tyr	Leu 215	Tyr	Ala	Asn	Ile	Cys 220	Phe	Arg	His	His
Glu 225	Thr	Ser	Gly	Ser	Val 230	Pro	Thr	Asp	Tyr	Leu 235	Gln	Leu	Met	Val	Tyr 240
Val	Val	Lys	Thr	Ser 245	Ile	Lys	Ile	Pro	Ser 250	Ser	His	Asn	Leu	Met 255	Lys
Gly	Gly	Ser	Thr 260	Lys	Asn	Trp	Ser	Gly 265	Asn	Ser	Glu	Phe	His 270	Phe	Tyr
Ser	Ile	Asn 275	Val	Gly	Gly	Phe	Phe 280	Lys	Leu	Arg	Ala	Gly 285	Glu	Glu	Ile

# Rede Fire